



SEQUENCE LISTING

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DEC 07 2001
TECH CENTER 1600/2900

<110> The General Hospital Corporation

<120> Rapid Immunoselection Cloning Method

<130> 11-88L

<140> US 09/836,544

<141> 2001-04-17

<150> US 07/983,647

<151> 1992-12-01

<150> US 07/553,759

<151> 1990-07-13

<150> US 07/498,809

<151> 1990-03-23

<150> US 07/379,076

<151> 1989-07-13

<150> US 07/160,416

<151> 1988-02-25

<160> 37

<170> PatentIn Ver. 2.0

<210> 1

<211> 2932

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Nucleotide
sequence of expression vector, pIH3

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<222> (7)..(1059)

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ttc aat gtt tct tcc aaa ggt gca gtc tcc aaa gag att acg aat gcc 96
Phe Asn Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala
15 20 25 30
ttg gaa acc tgg ggt gcc ttg ggt cag gac atc aac ttg gac att cct 144
Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro
35 40 45
agt ttt caa atg agt gat gat att gac gat ata aaa tgg gaa aaa act 192
Ser Phe Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr
50 55 60

tca gac aag aaa aag att gca caa ttc aga aaa gag aaa gag act ttc	240
Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe	
65 70 75	
aag gaa aaa gat aca tat aag cta ttt aaa aat gga act ctg aaa att	288
Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile	
80 85 90	
aag cat ctg aag acc gat gat cag gat atc tac aag gta tca ata tat	336
Lys His Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr	
95 100 105 110	
gat aca aaa gga aaa aat gtg ttg gaa aaa ata ttt gat ttg aag att	384
Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile	
115 120 125	
caa gag agg gtc tca aaa cca aag atc tcc tgg act tgt atc aac aca	432
Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr	
130 135 140	
acc ctg acc tgt gag gta atg aat gga act gac ccc gaa tta aac ctg	480
Thr Leu Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu	
145 150 155	
tat caa gat ggg aaa cat cta aaa ctt tct cag agg gtc atc aca cac	528
Tyr Gln Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His	
160 165 170	
aag tgg acc acc agc ctg agt gca aaa ttc aag tgc aca gca ggg aac	576
Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn	
175 180 185 190	
aaa gtc agc aag gaa tcc agt gtc gag cct gtc agc tgt cca gag aaa	624
Lys Val Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys	
195 200 205	
ggg ctg gac atc tat ctc atc att ggc ata tgt gga gga ggc agc ctc	672
Gly Leu Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu	
210 215 220	
ttg atg gtc ttt gtg gca ctg ctc gtt ttc tat atc acc aaa agg aaa	720
Leu Met Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys	
225 230 235	
aaa cag agg agt cgg aga aat gat gag gag ctg gag aca aga gcc cac	768
Lys Gln Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His	
240 245 250	
aga gta gct act gaa gaa agg ggc cgg aag ccc cac caa att cca gct	816
Arg Val Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala	
255 260 265 270	
tca acc cct cag aat cca gca act tcc caa cat cct cct cca cca cct	864
Ser Thr Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro	
275 280 285	

ggt cat cgt tcc cag gca cct agt cat cgt ccc ccg cct cct gga cac 912
 Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His
 290 295 300

cgt gtt cag cac cag cct cag aag agg cct cct gct ccg tcg ggc aca 960
 Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr
 305 310 315

caa gtt cac cag cag aaa ggc ccg ccc ctc ccc aga cct cga gtt cag 1008
 Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln
 320 325 330

cca aaa cct ccc cat ggg gca gca gaa aac tca ttg tcc cct tcc tct 1056
 Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser
 335 340 345 350

aat taataaagat agaaactgtc tttttcaata aaaagcactg tggatttctg 1109
 Asn

ccctcctgat gtgcatatcc gtacttccat gaggtgtttt ctgtgtgcag aacattgtca 1169
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 35 40 45

Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
 50 55 60

Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
 65 70 75 80

Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
 85 95
 Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
 100 105 110
 Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
 115 120 125
 Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
 130 135 140
 Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
 145 150 155 160
 Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
 165 170 175
 Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
 180 185 190
 Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
 195 200 205
 Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met
 210 215 220
 Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln
 225 230 235 240
 Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val
 245 250 255
 Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr
 260 265 270
 Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro Gly His
 275 280 285
 Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val
 290 295 300
 Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
 305 310 315 320
 His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys
 325 330 335
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 340 345 350

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<220>
 <221> CDS
 <222> (13)..(723)

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 Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe
 15 20 25

tcc caa caa ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta 147
 Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val
 30 35 40 45

cca agc aat gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat 195
 Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp
 50 55 60

aaa gtt gca gaa ctg gaa aat tct gaa ttc aga gct ttc tca tct ttt 243
 Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe
 65 70 75

aaa aat agg gtt tat tta gac act gtg tca ggt agc ctc act atc tac 291
 Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr
 80 85 90

aac tta aca tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat 339
 Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn
 95 100 105

att act gat acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca 387
 Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro
 110 115 120 125

tct ccc aca cta act tgt gca ttg act aat gga agc att gaa gtc caa 435
 Ser Pro Thr Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln
 130 135 140

tgc atg ata cca gag cat tac aac agc cat cga gga ctt ata atg tac 483
 Cys Met Ile Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr
 145 150 155

tca tgg gat tgt cct atg gag caa tgt aaa cgt aac tca acc agt ata 531
 Ser Trp Asp Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile
 160 165 170

tat ttt aag atg gaa aat gat ctt cca caa aaa ata cag tgt act ctt 579

Tyr Phe Lys Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu
 175 180 185
 agc aat cca tta ttt aat aca aca tca tca atc att ttg aca acc tgt 627
 Ser Asn Pro Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys
 190 195 200 205
 atc cca agc agc ggt cat tca aga cac aga tat gca ctt ata ccc ata 675
 Ile Pro Ser Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile
 210 215 220
 cca tta gca gta att aca aca tgt att gtg ctg tat atg aat gtt ctt 723
 Pro Leu Ala Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Val Leu
 225 230 235
 taattgagaa gacaatttct tcatttttag gtattctgaa atgtgacaga aaaccagaca 783
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 <213> Homo sapiens

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 35 40 45
 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
 50 55 60
 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
 65 70 75 80
 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
 85 90 95
 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
 100 105 110
 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
 115 120 125
 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
 130 135 140

Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
 145 150 155 160
 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
 165 170 175
 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
 180 185 190
 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
 195 200 205
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 210 215 220
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 225 230 235

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Nucleotide
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 cccatggctg actaattttt tttatttatg cagaggccga ggccgcctcg gcctctgagc 3840
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 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (100)..(759)

<400> 7

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Met Leu Arg Leu Leu
1 5

ttg gct ctc aac tta ttc cct tca att caa gta aca gga aac aag att 162
Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val Thr Gly Asn Lys Ile
10 15 20

ttg gtg aag cag tcg ccc atg ctt gta gcg tac gac aat gcg gtc aac 210
Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr Asp Asn Ala Val Asn
25 30 35

ctt agc tgc aag tat tcc tac aat ctc ttc tca agg gag ttc cgg gca 258
Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser Arg Glu Phe Arg Ala
40 45 50

tcc ctt cac aaa gga ctg gat agt gct gtg gaa gtc tgt gtt gta tat 306
Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys Val Val Tyr
55 60 65

ggg aat tac tcc cag cag ctt cag gtt tac tca aaa acg ggg ttc aac 354
Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser Lys Thr Gly Phe Asn
70 75 80 85

tgt gat ggg aaa ttg ggc aat gaa tca gtg aca ttc tac ctc cag aat 402
Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr Phe Tyr Leu Gln Asn
90 95 100

ttg tat gtt aac caa aca gat att tac ttc tgc aaa att gaa gtt atg 450
Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys Lys Ile Glu Val Met
105 110 115

tat cct cct cct tac cta gac aat gag aag agc aat gga acc att atc 498
Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile
120 125 130

cat gtg aaa ggg aaa cac ctt tgt cca agt ccc cta ttt ccc gga cct 546
His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro
135 140 145

tct aag ccc ttt tgg gtg ctg gtg gtg gtt ggt gga gtc ctg gct tgc 594
Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
150 155 160 165

tat agc ttg cta gta aca gtg gcc ttt att att ttc tgg gtg agg agt 642
Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
170 175 180

aag agg agc agg ctc ctg cac agt gac tac atg aac atg act ccc cgc 690
Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
185 190 195
cgc ccc ggg ccc acc cgc aag cat tac cag ccc tat gcc cca cca cgc 738
Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg
200 205 210
gac ttc gca gcc tat cgc tcc tgacacggac gcctatccag aagccagccg 789
Asp Phe Ala Ala Tyr Arg Ser
215 220
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ggatttggtc aaatgagggg ttcctcaaaa gcaatatcag gtaaaccaag ttgctttcct 1449
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agttc 1514

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<212> PRT
<213> Homo sapiens

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Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
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Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
35 40 45
Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu

50	55	60
Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser		
65	70	75
Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr		
	85	90
Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys		
	100	105
Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser		
	115	120
Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro		
	130	135
Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly		
	145	150
Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile		
	165	170
Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met		
	180	185
Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro		
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Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser		
	210	215

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 <212> DNA
 <213> Homo sapiens

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 tctccctgcc ccatgagctc agagcccca gtctgagcca cagcacagcc cccaggaagc 240
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 ggacccggtg gggagtggcc ggggctgtcc aggcagggcc gctgctttgg gaggaagaag 360
 cccacagtct cggaacacga ggacagcacc tcccccaaca ccacagccgg tgcccagatc 420
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ggccccacca tccccaccac tgtccccctgc agggaggaca ttctctgtcc ttctggccag 540
 actgatggtg acagcccagg tcctcccaga ggtgcagcag tctccccact gcacgactgt 600
 ccccgtagga gcctccgtca acatcacctg ctccaccagc gggggcctgc gtgggatcta 660
 cctgaggcag ctggggccac agccccaaga catcatttac tacgaggacg gggtagtgcc 720
 cactacggac agacggttcc ggggccgcat cgactttctca ggggtcccagg acaacctgac 780
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 atggcacaga tgctcggacg cccaccaag ggcctctgcc ctccctgccc caccgacagg 960
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 gtaccagtga cccagtgggc cctgcacgt ccgcctgtg gtccccccag caccttcct 1260
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 ttgagcccc gtggatcaac gtgtccagg aggactctgt gactctgaca tgccaggggg 180
 ctgcagccc tgagagcgac tccattcagt ggttcacaa tgggaatctc attcccacc 240

acacgcagcc cagctacagg ttcaaggcca acaacaatga cagcggggag tacacgtgcc 300
 agactggcca gaccagcctc agcgaccctg tgcattctgac tgtgctttcc gaatggctgg 360
 tgctccagac ccctcacctg gagttccagg agggagaaac catcatgctg aggtgccaca 420
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 tctcccgttt ggatcccacc ttctccatcc cacaagcaaa ccacagtcac agtggtgatt 540
 accactgcac aggaaacata ggctacacgc tgttctcatc caagcctgtg accatcactg 600
 tccaagtgcc cagcatgggc agctcttcac caatggggat cattgtggct gtggtcattg 660
 cgactgctgt agcagccatt gttgctgctg tagtggcctt gatctactgc aggaaaaagc 720
 ggatttcagc caattccact gatcctgtga aggctgccc aattgagcca cctggacgtc 780
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 tgactcttcc tccaacgac catgtcaaca gtaataacta aagagtaacg ttatgccatg 960
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 taactttgct taaactacaa acacaagcaa aacttcacgg ggtcatacta catacaagca 1140
 taagcaaaac ttaacttggga tcatttctgg taaatgctta tgttagaaat aagacaacc 1200
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 ttcactgctt atgcagtcgg aagctccaga agaacaaaga gcccaattac cagaaccaca 1860
 ttaagtctcc attgttttgc cttgggattt gagaagagaa ttagagaggt gaggatctgg 1920

acg gag aaa aac tcc agg aag tgt ttg gtc aaa gga aaa atg ata atg 450
 Thr Glu Lys Asn Ser Arg Lys Cys Leu Val Lys Gly Lys Met Ile Met
 105 110 115

aat tca ttg agc ctc ttt gct gcc att tct gga atg att ctt tca atc 498
 Asn Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser Ile
 120 125 130 135

atg gac ata ctt aat att aaa att tcc cat ttt tta aaa atg gag agt 546
 Met Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys Met Glu Ser
 140 145 150

ctg aat ttt att aga gct cac aca cca tat att aac ata tac aac tgt 594
 Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys
 155 160 165

gaa cca gct aat ccc tct gag aaa aac tcc cca tct acc caa tac tgt 642
 Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys
 170 175 180

tac agc ata caa tct ctg ttc ttg ggc att ttg tca gtg atg ctg atc 690
 Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu Ile
 185 190 195

ttt gcc ttc ttc cag gaa ctt gta ata gct ggc atc gtt gag aat gaa 738
 Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn Glu
 200 205 210 215

tgg aaa aga acg tgc tcc aga ccc aaa tct aac ata gtt ctc ctg tca 786
 Trp Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile Val Leu Leu Ser
 220 225 230

gca gaa gaa aaa aaa gaa cag act att gaa ata aaa gaa gaa gtg gtt 834
 Ala Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys Glu Glu Val Val
 235 240 245

ggg cta act gaa aca tct tcc caa cca aag aat gaa gaa gac att gaa 882
 Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu Glu Asp Ile Glu
 250 255 260

att att cca atc caa gaa gag gaa gaa gaa gaa aca gag acg aac ttt 930
 Ile Ile Pro Ile Gln Glu Glu Glu Glu Glu Glu Thr Glu Thr Asn Phe
 265 270 275

cca gaa cct ccc caa gat cag gaa tcc tca cca ata gaa aat gac agc 978
 Pro Glu Pro Pro Gln Asp Gln Glu Ser Ser Pro Ile Glu Asn Asp Ser
 280 285 290 295

tct cct taagtgtttt cttctgtttt ctgtttcctt ttttaaacat tagtgttcat 1034
 Ser Pro

agcttccaag agacatgctg actttcattt cttgaggtac tctgcacata cgcaccacat 1094

ctctatctgg cctttgcatg gagtgaccat agctccttct ctcttacatt gaatgtagag 1154

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 <212> PRT
 <213> Homo sapiens

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 Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
 35 40 45
 Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
 50 55 60
 Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
 65 70 75 80
 Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
 85 90 95
 Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
 100 105 110
 Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
 115 120 125
 Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
 130 135 140
 His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
 145 150 155 160
 Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
 165 170 175
 Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
 180 185 190

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
 195 200 205

Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
 210 215 220

Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
 225 230 235 240

Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
 245 250 255

Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu
 260 265 270

Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
 275 280 285

Ser Pro Ile Glu Asn Asp Ser Ser Pro
 290 295

<210> 13
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> (13)..(1608)

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 Leu Val Leu Leu Gly Ala Leu Phe Pro Gly Pro Gly Asn Ala Gln Thr
 15 20 25

tct gtg tcc ccc tca aaa gtc atc ctg ccc cgg gga ggc tcc gtg ctg 147
 Ser Val Ser Pro Ser Lys Val Ile Leu Pro Arg Gly Gly Ser Val Leu
 30 35 40 45

gtg aca tgc agc acc tcc tgt gac cag ccc aag ttg ttg ggc ata gag 195
 Val Thr Cys Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly Ile Glu
 50 55 60

acc ccg ttg cct aaa aag gag ttg ctc ctg cct ggg aac aac cgg aag 243
 Thr Pro Leu Pro Lys Lys Glu Leu Leu Leu Pro Gly Asn Asn Arg Lys
 65 70 75

gtg tat gaa ctg agc aat gtg caa gaa gat agc caa cca atg tgc tat	291
Val Tyr Glu Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met Cys Tyr	
80 85 90	
tca aac tgc cct gat ggg cag tca aca gct aaa acc ttc ctc acc gtg	339
Ser Asn Cys Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu Thr Val	
95 100 105	
tac tgg act cca gaa cgg gtg gaa ctg gca ccc ctc ccc tct tgg cag	387
Tyr Trp Thr Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser Trp Gln	
110 115 120 125	
cca gtg ggc aag aac ctt acc cta cgc tgc cag gtg gag ggt ggg gca	435
Pro Val Gly Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly Gly Ala	
130 135 140	
ccc cgg gcc aac ctc acc gtg gtg ctg ctc cgt ggg gag aag gag ctg	483
Pro Arg Ala Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu	
145 150 155	
aaa cgg gag cca gct gtg ggg gag ccc gct gag gtc acg acc acg gtg	531
Lys Arg Glu Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Thr Val	
160 165 170	
ctg gtg agg aga gat cac cat gga gcc aat ttc tcg tgc cgc act gaa	579
Leu Val Arg Arg Asp His His Gly Ala Asn Phe Ser Cys Arg Thr Glu	
175 180 185	
ctg gac ctg cgg ccc caa ggg ctg gag ctg ttt gag aac acc tcg gcc	627
Leu Asp Leu Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr Ser Ala	
190 195 200 205	
ccc tac cag ctc cag acc ttt gtc ctg cca gcg act ccc cca caa ctt	675
Pro Tyr Gln Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro Gln Leu	
210 215 220	
gtc agc ccc cgg gtc cta gag gtg gac acg cag ggg acc gtg gtc tgt	723
Val Ser Pro Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val Cys	
225 230 235	
tcc ctg gac ggg ctg ttc cca gtc tcg gag gcc cag gtc cac ctg gca	771
Ser Leu Asp Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala	
240 245 250	
ctg ggg gac cag agg ttg aac ccc aca gtc acc tat ggc aac gac tcc	819
Leu Gly Asp Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser	
255 260 265	
ttc tcg gcc aag gcc tca gtc agt gtg acc gca gag gac gag ggc acc	867
Phe Ser Ala Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr	
270 275 280 285	
cag cgg ctg acg tgt gca gta ata ctg ggg aac cag agc cag gag aca	915
Gln Arg Leu Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr	
290 295 300	

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acg aag cca gag gtc tca gaa ggg acc gag gtg aca gtg aag tgt gag Thr Lys Pro Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys Cys Glu 320 325 330	1011
gcc cac cct aga gcc aag gtg acg ctg aat ggg gtt cca gcc cag cca Ala His Pro Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala Gln Pro 335 340 345	1059
ctg ggc ccg agg gcc cag ctc ctg ctg aag gcc acc cca gag gac aac Leu Gly Pro Arg Ala Gln Leu Leu Lys Ala Thr Pro Glu Asp Asn 350 355 360 365	1107
ggg cgc agc ttc tcc tgc tct gca acc ctg gag gtg gcc ggc cag ctt Gly Arg Ser Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly Gln Leu 370 375 380	1155
ata cac aag aac cag acc cgg gag ctt cgt gtc ctg tat ggc ccc cga Ile His Lys Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly Pro Arg 385 390 395	1203
ctg gac gag agg gat tgt ccg gga aac tgg acg tgg cca gaa aat tcc Leu Asp Glu Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu Asn Ser 400 405 410	1251
cag cag act cca atg tgc cag gct tgg ggg aac cca ttg ccc gag ctc Gln Gln Thr Pro Met Cys Gln Ala Trp Gly Asn Pro Leu Pro Glu Leu 415 420 425	1299
aag tgt cta aag gat ggc act ttc cca ctg ccc atc ggg gaa tca gtg Lys Cys Leu Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu Ser Val 430 435 440 445	1347
act gtc act cga gat ctt gag ggc acc tac ctc tgt cgg gcc agg agc Thr Val Thr Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala Arg Ser 450 455 460	1395
act caa ggg gag gtc acc cgc gag gtg acc gtg aat gtg ctc tcc ccc Thr Gln Gly Glu Val Thr Arg Glu Val Thr Val Asn Val Leu Ser Pro 465 470 475	1443
cgg tat gag att gtc atc atc act gtg gta gca gcc gca gtc ata atg Arg Tyr Glu Ile Val Ile Ile Thr Val Val Ala Ala Ala Val Ile Met 480 485 490	1491
ggc act gca ggc ctc agc acg tac ctc tat aac cgc cag cgg aag atc Gly Thr Ala Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg Lys Ile 495 500 505	1539

aag aaa tac aga cta caa cag gcc caa aaa ggg acc ccc atg aaa ccg 1587
 Lys Lys Tyr Arg Leu Gln Gln Ala Gln Lys Gly Thr Pro Met Lys Pro
 510 515 520 525

aac aca caa gcc acg cct ccc tgaacctatc ccgggacagg gcctcttcct 1638
 Asn Thr Gln Ala Thr Pro Pro
 530

cggccttccc atattggtgg cagtgggtgcc aactgaaca gagtgggaaga catatgccat 1698
 gcagctacac ctaccggccc tgggacgccg gaggacaggg cattgtcctc agtcagatac 1758
 aacagcattt ggggccatgg tacctgcaca cctaaaacac taggccacgc atctgatctg 1818
 tagtcacatg actaagccaa gaggaaggaa cagcatttgg ggccatggta cctgcacacc 1878
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<210> 14
 <211> 532
 <212> PRT
 <213> Homo sapiens

<400> 14
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 20 25 30
 Pro Ser Lys Val Ile Leu Pro Arg Gly Gly Ser Val Leu Val Thr Cys
 35 40 45
 Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly Ile Glu Thr Pro Leu
 50 55 60
 Pro Lys Lys Glu Leu Leu Leu Pro Gly Asn Asn Arg Lys Val Tyr Glu
 65 70 75 80
 Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met Cys Tyr Ser Asn Cys
 85 90 95
 Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu Thr Val Tyr Trp Thr
 100 105 110
 Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser Trp Gln Pro Val Gly
 115 120 125
 Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly Gly Ala Pro Arg Ala
 130 135 140
 Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu Lys Arg Glu
 145 150 155 160

Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Thr Val Leu Val Arg
 165 170 175

Arg Asp His His Gly Ala Asn Phe Ser Cys Arg Thr Glu Leu Asp Leu
 180 185 190

Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr Ser Ala Pro Tyr Gln
 195 200 205

Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro Gln Leu Val Ser Pro
 210 215 220

Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val Cys Ser Leu Asp
 225 230 235 240

Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala Leu Gly Asp
 245 250 255

Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser Phe Ser Ala
 260 265 270

Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr Gln Arg Leu
 275 280 285

Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr Leu Gln Thr
 290 295 300

Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val Ile Leu Thr Lys Pro
 305 310 315 320

Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys Cys Glu Ala His Pro
 325 330 335

Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala Gln Pro Leu Gly Pro
 340 345 350

Arg Ala Gln Leu Leu Leu Lys Ala Thr Pro Glu Asp Asn Gly Arg Ser
 355 360 365

Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly Gln Leu Ile His Lys
 370 375 380

Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly Pro Arg Leu Asp Glu
 385 390 395 400

Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu Asn Ser Gln Gln Thr
 405 410 415

Pro Met Cys Gln Ala Trp Gly Asn Pro Leu Pro Glu Leu Lys Cys Leu
 420 425 430

Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu Ser Val Thr Val Thr
 435 440 445

Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala Arg Ser Thr Gln Gly
 450 455 460
 Glu Val Thr Arg Glu Val Thr Val Asn Val Leu Ser Pro Arg Tyr Glu
 465 470 475 480
 Ile Val Ile Ile Thr Val Val Ala Ala Ala Val Ile Met Gly Thr Ala
 485 490 495
 Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg Lys Ile Lys Lys Tyr
 500 505 510
 Arg Leu Gln Gln Ala Gln Lys Gly Thr Pro Met Lys Pro Asn Thr Gln
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 Ala Thr Pro Pro
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<210> 15
 <211> 1922
 <212> DNA
 <213> Homo sapiens

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 gctgcagtgc ctcaagggga cctcagatgg cccactcag cagctgacct ggtctcgga 180
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 gaggccccctg gccatctggc ttttcatctt caacgtctct caacagatgg ggggcttcta 300
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 gctgtatgtg tgggcccagg accgccctga gatctgggag ggagagcctc cgtgtgtccc 540
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 ccatgtgcac cccaaggggc ctaagtcatt gctgagccta gagctgaagg acgatcgccc 720
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 cgctggaaaag tattattgtc accgtggcaa cctgaccatg tcattccacc tggagatcac 840
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gactttggct tatctgatct tctgcctgtg ttcccttgtg ggcattcttc atcttcaaag 960
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 cacaccacc tcaggcctcg gacgcgcca gcgttgggcc gcaggcctgg ggggactgc 1140
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 ggggtccagt cctatgagga tatgagagga atcctgtatg cagccccca gctccgctcc 1560
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 aatcccgatg ggccagacct agcctgggga ggagggggcc gcatgggcac ctggagcacc 1680
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 gtgcatgtgt gtaagtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtat acatgccagt 1860
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 aa 1922

<210> 16
 <211> 1476
 <212> DNA
 <213> Homo sapiens

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 atgggacttt cccggcagag ccaatgaaag gccctattgc tatgcaatct ggtccaaaac 180
 cactcttcag gaggatgtct tcaactgggtg gccccacgca aagcttcttc atgagggaaat 240
 ctaagacttt gggggctgtc cagattatga atgggtcttt ccacattgcc ctgggggggtc 300
 ttctgatgat ccagcaggg atctatgcac ccactgtgtg gactgtgtgg taccctctct 360

ggggagggcat tatgtatatt atttccggat cactcctggc agcaacggag aaaaactcca 420
 ggaagtgttt ggtcaaagga aaaatgataa tgaattcatt gagcctcttt gctgccat 480
 ctggaatgat tctttcaatc atggacatac ttaatatata aatttcccat tttttaaaaa 540
 tggagagtct gaattttatt agagctcaca caccatatac taacatatac aactgtgaac 600
 cagctaatacc ctctgagaaa aactcccat ctaccaata ctgttacagc atacaatctc 660
 tgttcttggg cattttgtca gtgatgctga tctttgcctt cttccaggaa cttgtaatag 720
 ctggcatcgt tgagaatgaa tggaaaagaa cgtgctccag acccaaactc aacatagttc 780
 tcctgtcagc agaagaaaaa aaagaacaga ctattgaaat aaaagaagaa gtggttgggc 840
 taactgaaac atcttcccaa ccaagaatg aagaagacat tgaaattatt ccaatccaag 900
 aagaggaaga agaagaaaca gagacgaact ttccagaacc tcccaagat caggaatcct 960
 caccaataga aaatgacagc tctccttaag tgatttcttc tgttttctgt ttctttttt 1020
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 cacatacgca ccacatctct atctggcctt tgcatggagt gaccatagct ccttctctct 1140
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 aacctgttcc ttggataggc tttttagtat agtatTTTT tttgtcattt tctccatcag 1320
 caaccagga gactgcacct gatggaaaag atatatgact gcttcatgac attcctaaac 1380
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 caatgatgca aaagggcttt agagcacaat ggatct 1476

<210> 17
 <211> 2290
 <212> DNA
 <213> Homo sapiens

<400> 17
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 ttgagcccc gtggatcaac gtgctccagg aggactctgt gactctgaca tgccagggg 180
 ctgcagccc tgagagcgac tccattcagt ggttcacaa tgggaatctc attcccacc 240
 acacgcagcc cagctacagg ttcaaggcca acaacaatga cagcggggag tacacgtgcc 300

agactggcca gaccagcctc agcgaccctg tgcacatgac tgtgctttcc gaatggctgg 360
 tgetccagac ccctcacctg gagttccagg agggagaaac catcatgctg aggtgccaca 420
 gctggaagga caagcctctg gtcaaggtca cattcttcca gaatggaaaa tcccagaaat 480
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 accactgcac aggaacata ggctacacgc tgttctcatc caagcctgtg accatcactg 600
 tccaagtgcc cagcatgggc agctcttcac caatggggat cattgtggct gtggtcattg 660
 cgactgctgt agcagccatt gttgctgctg tagtggcctt gatctactgc aggaaaaagc 720
 ggatttcagc caattccact gatcctgtga aggtgccca atttgagcca cctggacgtc 780
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 acggcggcta catgactctg aaccccaggg cacctactga cgatgataaa aacatctacc 900
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 tggtcatact ctcagcttgc tgagtggatg aaaaaagag gggaattgtt aaaggaaaat 1020
 ttaaattggag actggaaaaa tcctgagcaa aaaaaaccac ctggccctta gaaatagctt 1080
 taactttgct taaactacaa acacaagcaa aacttcacgg ggtcatacta catacaagca 1140
 taagcaaac ttaacttga tcatttctgg taaatgctta tggtagaat aagacaacc 1200
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 ttaagtctcc attgttttgc cttgggattt gagaagagaa ttagagaggt gaggatctgg 1920
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aggactcttc cagagtcatc tacctgagtc ccaaagctcc ctgtcctgaa agccacagac 2040
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tcttctgttc cacatccaca cagccaatac aattagtcaa accactgtta ttaacagatg 2160
tagcaacatg agaaacgctt atgttacagg ttacatgaga gcaatcatgt aagtctatat 2220
gacttcagaa atgttaaaat agactaacct ctaacaacaa attaaaagtg attgtttcaa 2280
ggtgaaaaaa 2290

<210> 18
<211> 2171
<212> DNA
<213> Homo sapiens

<400> 18
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tcatatgctt ctgtggacag ctgtgctatc cctggctcct gttgctggga cacctgcagc 180
tcccccaaag gctgtgctga aactcgagcc ccagtggatc aacgtgctcc aggaggactc 240
tgtgactctg acatgcgggg ggactcacag ccctgagagc gactccattc agtggttcca 300
caatgggaat ctcatcccca cccacacgca gccagctac aggttcaagg ccaacaacaa 360
tgacagcggg gagtacacgt gccagactgg ccagaccagc ctacagcagc ctgtgcatct 420
gactgtgctt tctggtcagt ggaggaaggc cccaggggtg acctgggagg gccaggacgg 480
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tatcgctgtg agttgcctca gcacatatca gtgggttgtt ttgcctcagt tctgattgaa 600
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cctactgcat aaaaccatt tccattttta tggcagaatt gaaaagcaca gaccacaact 720
gaatcctagc cctggaaatg actcactata caacatgatg aattcattta acccttgagt 780
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tgtcttacc atctttgtat ttccagcatc tgaaactggg cagagcttaa taaatatttt 1020
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gttacaatga gattgtgatg aacattgtcc ttgtggcttt tcacttagtc ccctcccttc 1140
 acctgaagag caaattttcc tcaaaagtac acagcaaacg aatgaccac tggtgacact 1200
 gttgccttta gaccctgctg gaaagaagct ccacatttat taacattccc gaagtaaatt 1260
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 aaaggcatat gtccttatca tatgaggact cctcggtcac actggattct tcctccctc 1380
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 <211> 1004
 <212> DNA
 <213> Homo sapiens

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 catgcagaga aaaacagtac ctaataaaca gtcagtgtgt ttctttgtgc cagccaggac 180
 agaaactggg gactgactgc acagagttca ctgaaacgga atgccttcct tgcggtgaaa 240
 gcgaattcct agacacctgg aacagagaga cacactgcca ccagcacaaa tactgagacc 300

caa gtt gtc ctc gaa gaa ggt aca att gct ttt aaa aat tgg gtt aaa 378
 Gln Val Val Leu Glu Glu Gly Thr Ile Ala Phe Lys Asn Trp Val Lys
 45 50 55

aca ggc aca gaa gtt tac aga cag ttt tgg atc ttt gat gtg caa aat 426
 Thr Gly Thr Glu Val Tyr Arg Gln Phe Trp Ile Phe Asp Val Gln Asn
 60 65 70

cca cag gaa gtg atg atg aac agc agc aac att caa gtt aag caa aga 474
 Pro Gln Glu Val Met Met Asn Ser Ser Asn Ile Gln Val Lys Gln Arg
 75 80 85

ggt cct tat acg tac aga gtt cgt ttt cta gcc aag gaa aat gta acc 522
 Gly Pro Tyr Thr Tyr Arg Val Arg Phe Leu Ala Lys Glu Asn Val Thr
 90 95 100

cag gac gct gag gac aac aca gtc tct ttc ctg cag ccc aat ggt gcc 570
 Gln Asp Ala Glu Asp Asn Thr Val Ser Phe Leu Gln Pro Asn Gly Ala
 105 110 115 120

atc ttc gaa cct tca cta tca gtt gga aca gag gct gac aac ttc aca 618
 Ile Phe Glu Pro Ser Leu Ser Val Gly Thr Glu Ala Asp Asn Phe Thr
 125 130 135

gtt ctc aat ctg gct gtg gca gct gca tcc cat atc tat caa aat caa 666
 Val Leu Asn Leu Ala Val Ala Ala Ser His Ile Tyr Gln Asn Gln
 140 145 150

ttt gtt caa atg atc ctc aat tca ctt att aac aag tca aaa tct tct 714
 Phe Val Gln Met Ile Leu Asn Ser Leu Ile Asn Lys Ser Lys Ser Ser
 155 160 165

atg ttc caa gtc aga act ttg aga gaa ctg tta tgg ggc tat agg gat 762
 Met Phe Gln Val Arg Thr Leu Arg Glu Leu Leu Trp Gly Tyr Arg Asp
 170 175 180

cca ttt ttg agt ttg gtt ccg tac cct gtt act acc aca gtt ggt ctg 810
 Pro Phe Leu Ser Leu Val Pro Tyr Pro Val Thr Thr Thr Val Gly Leu
 185 190 195 200

ttt tat cct tac aac aat act gca gat gga gtt tat aaa gtt ttc aat 858
 Phe Tyr Pro Tyr Asn Asn Thr Ala Asp Gly Val Tyr Lys Val Phe Asn
 205 210 215

gga aaa gat aac ata agt aaa gtt gcc ata atc gac aca tat aaa ggt 906
 Gly Lys Asp Asn Ile Ser Lys Val Ala Ile Ile Asp Thr Tyr Lys Gly
 220 225 230

aaa agg aat ctg tcc tat tgg gaa agt cac tgc gac atg att aat ggt 954
 Lys Arg Asn Leu Ser Tyr Trp Glu Ser His Cys Asp Met Ile Asn Gly
 235 240 245

aca gat gca gcc tca ttt cca cct ttt gtt gag aaa agc cag gta ttg 1002
 Thr Asp Ala Ala Ser Phe Pro Pro Phe Val Glu Lys Ser Gln Val Leu
 250 255 260

cag ttc ttt tct tct gat att tgc agg tca atc tat gct gta ttt gaa 1050
 Gln Phe Phe Ser Ser Asp Ile Cys Arg Ser Ile Tyr Ala Val Phe Glu
 265 270 275 280

tcc gac gtt aat ctg aaa gga atc cct gtg tat aga ttt gtt ctt cca 1098
 Ser Asp Val Asn Leu Lys Gly Ile Pro Val Tyr Arg Phe Val Leu Pro
 285 290 295

tcc aag gcc ttt gcc tct cca gtt gaa aac cca gac aac tat tgt ttc 1146
 Ser Lys Ala Phe Ala Ser Pro Val Glu Asn Pro Asp Asn Tyr Cys Phe
 300 305 310

tgc aca gaa aaa att atc tca aaa aat tgt aca tca tat ggt gtg cta 1194
 Cys Thr Glu Lys Ile Ile Ser Lys Asn Cys Thr Ser Tyr Gly Val Leu
 315 320 325

gac atc agc aaa tgc aaa gaa ggg aga cct gtg tac att tca ctt cct 1242
 Asp Ile Ser Lys Cys Lys Glu Gly Arg Pro Val Tyr Ile Ser Leu Pro
 330 335 340

cat ttt ctg tat gca agt cct gat gtt tca gaa cct att gat gga tta 1290
 His Phe Leu Tyr Ala Ser Pro Asp Val Ser Glu Pro Ile Asp Gly Leu
 345 350 355 360

aac cca aat gaa gaa gaa cat agg aca tac ttg gat att gaa cct ata 1338
 Asn Pro Asn Glu Glu Glu His Arg Thr Tyr Leu Asp Ile Glu Pro Ile
 365 370 375

act gga ttc act tta caa ttt gca aaa cgg ctg cag gtc aac cta ttg 1386
 Thr Gly Phe Thr Leu Gln Phe Ala Lys Arg Leu Gln Val Asn Leu Leu
 380 385 390

gtc aag cca tca gaa aaa att caa gta tta aag aat ctg aag agg aac 1434
 Val Lys Pro Ser Glu Lys Ile Gln Val Leu Lys Asn Leu Lys Arg Asn
 395 400 405

tat att gtg cct att ctt tgg ctt aat gag act ggg acc att ggt gat 1482
 Tyr Ile Val Pro Ile Leu Trp Leu Asn Glu Thr Gly Thr Ile Gly Asp
 410 415 420

gag aag gca aac atg ttc aga agt caa gta act gga aaa ata aac ctc 1530
 Glu Lys Ala Asn Met Phe Arg Ser Gln Val Thr Gly Lys Ile Asn Leu
 425 430 435 440

ctt ggc ctg ata gaa atg atc tta ctc agt gtt ggt gtg gtg atg ttt 1578
 Leu Gly Leu Ile Glu Met Ile Leu Leu Ser Val Gly Val Val Met Phe
 445 450 455

gtt gct ttt atg att tca tat tgt gca tgc aga tcg aaa aca ata aaa 1626
 Val Ala Phe Met Ile Ser Tyr Cys Ala Cys Arg Ser Lys Thr Ile Lys
 460 465 470

taagtatgta ccaaaaaata ttgcttcaat aatattagct tatatattac ttgttttcac 1686

tttatcaaag agaagttaca tattaggcca tatatatttc tagacatgtc tagccactga 1746
 tcatttttaa atataggtaa ataaacctat aaatattatc acgcagatca ctaaagtata 1806
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 aaat 1870

<210> 21
 <211> 472
 <212> PRT
 <213> Homo sapiens

<400> 21
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 Leu Ile Gln Lys Thr Ile Lys Lys Gln Val Val Leu Glu Glu Gly Thr
 35 40 45
 Ile Ala Phe Lys Asn Trp Val Lys Thr Gly Thr Glu Val Tyr Arg Gln
 50 55 60
 Phe Trp Ile Phe Asp Val Gln Asn Pro Gln Glu Val Met Met Asn Ser
 65 70 75 80
 Ser Asn Ile Gln Val Lys Gln Arg Gly Pro Tyr Thr Tyr Arg Val Arg
 85 90 95
 Phe Leu Ala Lys Glu Asn Val Thr Gln Asp Ala Glu Asp Asn Thr Val
 100 105 110
 Ser Phe Leu Gln Pro Asn Gly Ala Ile Phe Glu Pro Ser Leu Ser Val
 115 120 125
 Gly Thr Glu Ala Asp Asn Phe Thr Val Leu Asn Leu Ala Val Ala Ala
 130 135 140
 Ala Ser His Ile Tyr Gln Asn Gln Phe Val Gln Met Ile Leu Asn Ser
 145 150 155 160
 Leu Ile Asn Lys Ser Lys Ser Ser Met Phe Gln Val Arg Thr Leu Arg
 165 170 175
 Glu Leu Leu Trp Gly Tyr Arg Asp Pro Phe Leu Ser Leu Val Pro Tyr
 180 185 190
 Pro Val Thr Thr Thr Val Gly Leu Phe Tyr Pro Tyr Asn Asn Thr Ala
 195 200 205

Asp Gly Val Tyr Lys Val Phe Asn Gly Lys Asp Asn Ile Ser Lys Val
 210 215 220
 Ala Ile Ile Asp Thr Tyr Lys Gly Lys Arg Asn Leu Ser Tyr Trp Glu
 225 230 235 240
 Ser His Cys Asp Met Ile Asn Gly Thr Asp Ala Ala Ser Phe Pro Pro
 245 250 255
 Phe Val Glu Lys Ser Gln Val Leu Gln Phe Phe Ser Ser Asp Ile Cys
 260 265 270
 Arg Ser Ile Tyr Ala Val Phe Glu Ser Asp Val Asn Leu Lys Gly Ile
 275 280 285
 Pro Val Tyr Arg Phe Val Leu Pro Ser Lys Ala Phe Ala Ser Pro Val
 290 295 300
 Glu Asn Pro Asp Asn Tyr Cys Phe Cys Thr Glu Lys Ile Ile Ser Lys
 305 310 315 320
 Asn Cys Thr Ser Tyr Gly Val Leu Asp Ile Ser Lys Cys Lys Glu Gly
 325 330 335
 Arg Pro Val Tyr Ile Ser Leu Pro His Phe Leu Tyr Ala Ser Pro Asp
 340 345 350
 Val Ser Glu Pro Ile Asp Gly Leu Asn Pro Asn Glu Glu Glu His Arg
 355 360 365
 Thr Tyr Leu Asp Ile Glu Pro Ile Thr Gly Phe Thr Leu Gln Phe Ala
 370 375 380
 Lys Arg Leu Gln Val Asn Leu Leu Val Lys Pro Ser Glu Lys Ile Gln
 385 390 395 400
 Val Leu Lys Asn Leu Lys Arg Asn Tyr Ile Val Pro Ile Leu Trp Leu
 405 410 415
 Asn Glu Thr Gly Thr Ile Gly Asp Glu Lys Ala Asn Met Phe Arg Ser
 420 425 430
 Gln Val Thr Gly Lys Ile Asn Leu Leu Gly Leu Ile Glu Met Ile Leu
 435 440 445
 Leu Ser Val Gly Val Val Met Phe Val Ala Phe Met Ile Ser Tyr Cys
 450 455 460
 Ala Cys Arg Ser Lys Thr Ile Lys
 465 470

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<220>
<221> CDS
<222> (37)..(1158)
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36

His Cys Ser Gly Met Gly Lys His Arg Tyr Thr Ser Ala Gly Ile Ser	
170	175 180
gtc act gtg aaa gag cta ttt cca gct cca gtg ctg aat gca tct gtg	630
Val Thr Val Lys Glu Leu Phe Pro Ala Pro Val Leu Asn Ala Ser Val	
185 190 195	
aca tcc cca ctc ctg gag ggg aat ctg gtc acc ctg agc tgt gaa aca	678
Thr Ser Pro Leu Leu Glu Gly Asn Leu Val Thr Leu Ser Cys Glu Thr	
200 205 210	
aag ttg ctc ttg cag agg cct ggt ttg cag ctt tac ttc tcc ttc tac	726
Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln Leu Tyr Phe Ser Phe Tyr	
215 220 225 230	
atg ggc agc aag acc ctg cga ggc agg aac aca tcc tct gaa tac caa	774
Met Gly Ser Lys Thr Leu Arg Gly Arg Asn Thr Ser Ser Glu Tyr Gln	
235 240 245	
ata cta act gct aga aga gaa gac tct ggg tta tac tgg tgc gag gct	822
Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly Leu Tyr Trp Cys Glu Ala	
250 255 260	
gcc aca gag gat gga aat gtc ctt aag cgc agc cct gag ttg gag ctt	870
Ala Thr Glu Asp Gly Asn Val Leu Lys Arg Ser Pro Glu Leu Glu Leu	
265 270 275	
caa gtg ctt ggc ctc cag tta cca act cct gtc tgg ttt cat gtc ctt	918
Gln Val Leu Gly Leu Gln Leu Pro Thr Pro Val Trp Phe His Val Leu	
280 285 290	
ttc tat ctg gca gtg gga ata atg ttt tta gtg aac act gtt ctc tgg	966
Phe Tyr Leu Ala Val Gly Ile Met Phe Leu Val Asn Thr Val Leu Trp	
295 300 305 310	
gtg aca ata cgt aaa gaa ctg aaa aga aag aaa aag tgg gat tta gaa	1014
Val Thr Ile Arg Lys Glu Leu Lys Arg Lys Lys Lys Trp Asp Leu Glu	
315 320 325	
atc tct ttg gat tct ggt cat gag aag aag gta act tcc agc ctt caa	1062
Ile Ser Leu Asp Ser Gly His Glu Lys Lys Val Thr Ser Ser Leu Gln	
330 335 340	
gaa gac aga cat tta gaa gaa gag ctg aaa tgt cag gaa caa aaa gaa	1110
Glu Asp Arg His Leu Glu Glu Glu Leu Lys Cys Gln Glu Gln Lys Glu	
345 350 355	
gaa cag ctg cag gaa ggg gtg cac cgg aag gag ccc cag ggg gcc acg	1158
Glu Gln Leu Gln Glu Gly Val His Arg Lys Glu Pro Gln Gly Ala Thr	
360 365 370	
tagcagcggc tcagtgggtg gccatcgatc tggaccgtcc cctgcccact tgctccccgt	1218
gagcactgcg tacaaacatc caaaagtcca acaacaccag aactgtgtgt ctcatggtat	1278

gtaactctta aagcaaataa atgaactgac ttcaaaaaaa aaa

1321

<210> 23
<211> 374
<212> PRT
<213> Homo sapiens

<400> 23
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1 5 10 15
Val Asp Thr Thr Lys Ala Val Ile Ser Leu Gln Pro Pro Trp Val Ser
20 25 30
Val Phe Gln Glu Glu Thr Val Thr Leu His Cys Glu Val Leu His Leu
35 40 45
Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln
50 55 60
Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser
65 70 75 80
Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile
85 90 95
Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg
100 105 110
Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys
115 120 125
Asp Lys Leu Val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe
130 135 140
Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile
145 150 155 160
Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr
165 170 175
Thr Ser Ala Gly Ile Ser Val Thr Val Lys Glu Leu Phe Pro Ala Pro
180 185 190
Val Leu Asn Ala Ser Val Thr Ser Pro Leu Leu Glu Gly Asn Leu Val
195 200 205
Thr Leu Ser Cys Glu Thr Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln
210 215 220
Leu Tyr Phe Ser Phe Tyr Met Gly Ser Lys Thr Leu Arg Gly Arg Asn
225 230 235 240

Thr Ser Ser Glu Tyr Gln Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly
 245 255
 Leu Tyr Trp Cys Glu Ala Ala Thr Glu Asp Gly Asn Val Leu Lys Arg
 260 265 270
 Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Leu Gln Leu Pro Thr Pro
 275 280 285
 Val Trp Phe His Val Leu Phe Tyr Leu Ala Val Gly Ile Met Phe Leu
 290 295 300
 Val Asn Thr Val Leu Trp Val Thr Ile Arg Lys Glu Leu Lys Arg Lys
 305 310 315 320
 Lys Lys Trp Asp Leu Glu Ile Ser Leu Asp Ser Gly His Glu Lys Lys
 325 330 335
 Val Thr Ser Ser Leu Gln Glu Asp Arg His Leu Glu Glu Glu Leu Lys
 340 345 350
 Cys Gln Glu Gln Lys Glu Glu Gln Leu Gln Glu Gly Val His Arg Lys
 355 360 365
 Glu Pro Gln Gly Ala Thr
 370

<210> 24
 <211> 1714
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (156)..(1163)

<400> 24
 gcggggagct tgcagtgacc aagaggggtgt tgaggctagg aggccacgat aaacaggata 60
 cgataaaagt ccttaaccaa gacgcagatg ggaagaagcg ttagagcgag cagcactcac 120
 atctcaagaa ccagcctttc aaacagtttc cagag atg gat tat cct act tta 173
 Met Asp Tyr Pro Thr Leu
 1 5
 ctt ttg gct ctt ctt cat gta tac aga gct cta tgt gaa gag gtg ctt 221
 Leu Leu Ala Leu Leu His Val Tyr Arg Ala Leu Cys Glu Glu Val Leu
 10 15 20
 tgg cat aca tca gtt ccc ttt gcc gag aac atg tct cta gaa tgt gtg 269
 Trp His Thr Ser Val Pro Phe Ala Glu Asn Met Ser Leu Glu Cys Val
 25 30 35

tat cca tca atg ggc atc tta aca cag gtg gag tgg ttc aag atc ggg Tyr Pro Ser Met Gly Ile Leu Thr Gln Val Glu Trp Phe Lys Ile Gly	317
40 45 50	
acc cag cag gat tcc ata gcc att ttc agc cct act cat ggc atg gtc Thr Gln Gln Asp Ser Ile Ala Ile Phe Ser Pro Thr His Gly Met Val	365
55 60 65 70	
ata agg aag ccc tat gct gag agg gtt tac ttt ttg aat tca acg atg Ile Arg Lys Pro Tyr Ala Glu Arg Val Tyr Phe Leu Asn Ser Thr Met	413
75 80 85	
gct tcc aat aac atg act ctt ttc ttt cgg aat gcc tct gaa gat gat Ala Ser Asn Asn Met Thr Leu Phe Phe Arg Asn Ala Ser Glu Asp Asp	461
90 95 100	
gtt ggc tac tat tcc tgc tct ctt tac act tac cca cag gga act tgg Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr Tyr Pro Gln Gly Thr Trp	509
105 110 115	
cag aag gtg ata cag gtg gtt cag tca gat agt ttt gag gca gct gtg Gln Lys Val Ile Gln Val Val Gln Ser Asp Ser Phe Glu Ala Ala Val	557
120 125 130	
cca tca aat agc cac att gtt tgc gaa cct gga aag aat gtc aca ctc Pro Ser Asn Ser His Ile Val Ser Glu Pro Gly Lys Asn Val Thr Leu	605
135 140 145 150	
act tgt cag cct cag atg acg tgg cct gtg cag gca gtg agg tgg gaa Thr Cys Gln Pro Gln Met Thr Trp Pro Val Gln Ala Val Arg Trp Glu	653
155 160 165	
aag atc cag ccc cgt cag atc gac ctc tta act tac tgc aac ttg gtc Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu Thr Tyr Cys Asn Leu Val	701
170 175 180	
cat ggc aga aat ttc acc tcc aag ttc cca aga caa ata gtg agc aac His Gly Arg Asn Phe Thr Ser Lys Phe Pro Arg Gln Ile Val Ser Asn	749
185 190 195	
tgc agc cac gga agg tgg agc gtc atc gtc atc ccc gat gtc aca gtc Cys Ser His Gly Arg Trp Ser Val Ile Val Ile Pro Asp Val Thr Val	797
200 205 210	
tca gac tgc ggg ctt tac cgc tgc tac ttg cag gcc agc gca gga gaa Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu Gln Ala Ser Ala Gly Glu	845
215 220 225 230	
aac gaa acc ttc gtg atg aga ttg act gta gcc gag ggt aaa acc gat Asn Glu Thr Phe Val Met Arg Leu Thr Val Ala Glu Gly Lys Thr Asp	893
235 240 245	
aac caa tat acc ctc ttt gtg gct gga ggg aca gtt tta ttg ttg ttg Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly Thr Val Leu Leu Leu	941
250 255 260	

ttt gtt atc tca att acc acc atc att gtc att ttc ctt aac aga agg 989
 Phe Val Ile Ser Ile Thr Thr Ile Ile Val Ile Phe Leu Asn Arg Arg
 265 270 275
 aga agg aga gag aga aga gat cta ttt aca gag tcc tgg gat aca cag 1037
 Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln
 280 285 290
 aag gca ccc aat aac tat aga agt ccc atc tct acc ggt caa cct acc 1085
 Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Gly Gln Pro Thr
 295 300 305 310
 aat caa tcc atg gat gat aca aga gag gat att tat gtc aac tat cca 1133
 Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr Val Asn Tyr Pro
 315 320 325
 acc ttc tct cgc aga cca aag act aga gtt taagcttatt cttgacatga 1183
 Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
 330 335
 gtgcattagt aatgactctt atgtactcat gcatggatct ttatgcaatt tttttccact 1243
 acccaaggtc taccttagat actagttgtc tgaattgagt tactttgata ggaaaaatac 1303
 ttcattacct aaaatcattt ttcatagaac tgtttcagaa aacctgactc taactgggtt 1363
 atatacaaaa gaaaacttac tgtatcatat aacagaatga tccaggggag attaagcttt 1423
 gggcaagggc tatttaccag ggcttaaatg ttgtgtctag aattaagtat gggcataaac 1483
 tggcttctga atccctttcc agagtgttgg atccatttcc ctggtcttgg cctcactctc 1543
 atgcaggctt tcctcttgtg ttggcaagat ggctgccaac tcttggcaat tcatacatcc 1603
 ttgtttctgt ctggtagaga gtttgcttct caaatggagc aaacaaattt gattatTTTT 1663
 tcattgttaa ataggcaaca tgaccataaa ggatggaatg gcttaagtaa a 1714

<210> 25
 <211> 336
 <212> PRT
 <213> Homo sapiens

<400> 25
 Met Asp Tyr Pro Thr Leu Leu Leu Ala Leu Leu His Val Tyr Arg Ala
 1 5 10 15
 Leu Cys Glu Glu Val Leu Trp His Thr Ser Val Pro Phe Ala Glu Asn
 20 25 30
 Met Ser Leu Glu Cys Val Tyr Pro Ser Met Gly Ile Leu Thr Gln Val
 35 40 45

Glu Trp Phe Lys Ile Gly Thr Gln Gln Asp Ser Ile Ala Ile Phe Ser
 50 55 60
 Pro Thr His Gly Met Val Ile Arg Lys Pro Tyr Ala Glu Arg Val Tyr
 65 70 75 80
 Phe Leu Asn Ser Thr Met Ala Ser Asn Asn Met Thr Leu Phe Phe Arg
 85 90 95
 Asn Ala Ser Glu Asp Asp Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr
 100 105 110
 Tyr Pro Gln Gly Thr Trp Gln Lys Val Ile Gln Val Val Gln Ser Asp
 115 120 125
 Ser Phe Glu Ala Ala Val Pro Ser Asn Ser His Ile Val Ser Glu Pro
 130 135 140
 Gly Lys Asn Val Thr Leu Thr Cys Gln Pro Gln Met Thr Trp Pro Val
 145 150 155 160
 Gln Ala Val Arg Trp Glu Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu
 165 170 175
 Thr Tyr Cys Asn Leu Val His Gly Arg Asn Phe Thr Ser Lys Phe Pro
 180 185 190
 Arg Gln Ile Val Ser Asn Cys Ser His Gly Arg Trp Ser Val Ile Val
 195 200 205
 Ile Pro Asp Val Thr Val Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu
 210 215 220
 Gln Ala Ser Ala Gly Glu Asn Glu Thr Phe Val Met Arg Leu Thr Val
 225 230 235 240
 Ala Glu Gly Lys Thr Asp Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly
 245 250 255
 Thr Val Leu Leu Leu Leu Phe Val Ile Ser Ile Thr Thr Ile Ile Val
 260 265 270
 Ile Phe Leu Asn Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr
 275 280 285
 Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile
 290 295 300
 Ser Thr Gly Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp
 305 310 315 320
 Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val
 325 330 335

<210> 26
 <211> 2107
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (35)..(1975)

<400> 26
 acgcggaac aggcttgac ccagacacga cacc atg cat ctc ctc ggc ccc tgg 55
 Met His Leu Leu Gly Pro Trp
 1 5

ctc ctg ctc ctg gtt cta gaa tac ttg gct ttc tct gac tca agt aaa 103
 Leu Leu Leu Leu Val Leu Glu Tyr Leu Ala Phe Ser Asp Ser Ser Lys
 10 15 20

tgg gtt ttt gag cac cct gaa acc ctc tac gcc tgg gag ggg gcc tgc 151
 Trp Val Phe Glu His Pro Glu Thr Leu Tyr Ala Trp Glu Gly Ala Cys
 25 30 35

gtc tgg atc ccc tgc acc tac aga gcc cta gat ggt gac ctg gaa agc 199
 Val Trp Ile Pro Cys Thr Tyr Arg Ala Leu Asp Gly Asp Leu Glu Ser
 40 45 50 55

ttc atc ctg ttc cac aat cct gag tat aac aag aac acc tcg aag ttt 247
 Phe Ile Leu Phe His Asn Pro Glu Tyr Asn Lys Asn Thr Ser Lys Phe
 60 65 70

gat ggg aca aga ctc tat gaa agc aca aag gat ggg aag gtt cct tct 295
 Asp Gly Thr Arg Leu Tyr Glu Ser Thr Lys Asp Gly Lys Val Pro Ser
 75 80 85

gag cag aaa agg gtg caa ttc ctg gga gac aag aat aag aac tgc aca 343
 Glu Gln Lys Arg Val Gln Phe Leu Gly Asp Lys Asn Lys Asn Cys Thr
 90 95 100

ctg agt atc cac ccg gtg cac ctc aat gac agt ggt cag ctg ggg ctg 391
 Leu Ser Ile His Pro Val His Leu Asn Asp Ser Gly Gln Leu Gly Leu
 105 110 115

agg atg gag tcc aag act gag aaa tgg atg gaa cga ata cac ctc aat 439
 Arg Met Glu Ser Lys Thr Glu Lys Trp Met Glu Arg Ile His Leu Asn
 120 125 130 135

gtc tct gaa agg cct ttt cca cct cat atc cag ctc cct cca gaa att 487
 Val Ser Glu Arg Pro Phe Pro Pro His Ile Gln Leu Pro Pro Glu Ile
 140 145 150

caa gag tcc cag gaa gtc act ctg acc tgc ttg ctg aat ttc tcc tgc 535
 Gln Glu Ser Gln Glu Val Thr Leu Thr Cys Leu Leu Asn Phe Ser Cys
 155 160 165

tat ggg tat ccg atc caa ttg cag tgg ctc cta gag ggg gtt cca atg Tyr Gly Tyr Pro Ile Gln Leu Gln Trp Leu Leu Glu Gly Val Pro Met 170 175 180	583
agg cag gct gct gtc acc tcg acc tcc ttg acc atc aag tct gtc ttc Arg Gln Ala Ala Val Thr Ser Thr Ser Leu Thr Ile Lys Ser Val Phe 185 190 195	631
acc cgg agc gag ctc aag ttc tcc cca cag tgg agt cac cat ggg aag Thr Arg Ser Glu Leu Lys Phe Ser Pro Gln Trp Ser His His Gly Lys 200 205 210 215	679
att gtg acc tgc cag ctt cag gat gca gat ggg aag ttc ctc tcc aat Ile Val Thr Cys Gln Leu Gln Asp Ala Asp Gly Lys Phe Leu Ser Asn 220 225 230	727
gac acg gtg cag ctg aac gtg aag cat cct ccc aag aag gtg acc aca Asp Thr Val Gln Leu Asn Val Lys His Pro Pro Lys Lys Val Thr Thr 235 240 245	775
gtg att caa aac ccc atg ccg att cga gaa gga gac aca gtg acc ctt Val Ile Gln Asn Pro Met Pro Ile Arg Glu Gly Asp Thr Val Thr Leu 250 255 260	823
tcc tgt aac tac aat tcc agt aac ccc agt gtt acc cgg tat gaa tgg Ser Cys Asn Tyr Asn Ser Ser Asn Pro Ser Val Thr Arg Tyr Glu Trp 265 270 275	871
aaa ccc cat ggc gcc tgg gag gag cca tcg ctt ggg gtg ctg aag atc Lys Pro His Gly Ala Trp Glu Glu Pro Ser Leu Gly Val Leu Lys Ile 280 285 290 295	919
caa aac gtt ggc tgg gac aac aca acc atc gcc tgc gca gct tgt aat Gln Asn Val Gly Trp Asp Asn Thr Thr Ile Ala Cys Ala Ala Cys Asn 300 305 310	967
agt tgg tgc tcg tgg gcc tcc cct gtc gcc ctg aat gtc cag tat gcc Ser Trp Cys Ser Trp Ala Ser Pro Val Ala Leu Asn Val Gln Tyr Ala 315 320 325	1015
ccc cga gac gtg agg gtc cgg aaa atc aag ccc ctt tcc gag att cac Pro Arg Asp Val Arg Val Arg Lys Ile Lys Pro Leu Ser Glu Ile His 330 335 340	1063
tct gga aac tcg gtc agc ctc caa tgt gac ttc tca agc agc cac ccc Ser Gly Asn Ser Val Ser Leu Gln Cys Asp Phe Ser Ser Ser His Pro 345 350 355	1111
aaa gaa gtc cag ttc ttc tgg gag aaa aat ggc agg ctt ctg ggg aaa Lys Glu Val Gln Phe Phe Trp Glu Lys Asn Gly Arg Leu Leu Gly Lys 360 365 370 375	1159
gaa agc cag ctg aat ttt gac tcc atc tcc cca gaa gat gct ggg agt Glu Ser Gln Leu Asn Phe Asp Ser Ile Ser Pro Glu Asp Ala Gly Ser 380 385 390	1207

tac agc tgc tgg gtg aac aac tcc ata gga cag aca gcg tcc aag gcc	1255
Tyr Ser Cys Trp Val Asn Asn Ser Ile Gly Gln Thr Ala Ser Lys Ala	
395 400 405	
tgg aca ctt gaa gtg ctg tat gca ccc agg agg ctg cgt gtg tcc atg	1303
Trp Thr Leu Glu Val Leu Tyr Ala Pro Arg Arg Leu Arg Val Ser Met	
410 415 420	
agc ccg ggg gac caa gtg atg gag ggg aag agt gca acc ctg acc tgt	1351
Ser Pro Gly Asp Gln Val Met Glu Gly Lys Ser Ala Thr Leu Thr Cys	
425 430 435	
gag agc gac gcc aac cct ccc gtc tcc cac tac acc tgg ttt gac tgg	1399
Glu Ser Asp Ala Asn Pro Pro Val Ser His Tyr Thr Trp Phe Asp Trp	
440 445 450 455	
aat aac caa agc ctc ccc tac cac agc cag aag ctg aga ttg gag ccg	1447
Asn Asn Gln Ser Leu Pro Tyr His Ser Gln Lys Leu Arg Leu Glu Pro	
460 465 470	
gtg aag gtc cag cac tcg ggt gcc tac tgg tgc cag ggg acc aac agt	1495
Val Lys Val Gln His Ser Gly Ala Tyr Trp Cys Gln Gly Thr Asn Ser	
475 480 485	
gtg ggc aag ggc cgt tcg cct ctc agc acc ctc acc gtc tac tat agc	1543
Val Gly Lys Gly Arg Ser Pro Leu Ser Thr Leu Thr Val Tyr Tyr Ser	
490 495 500	
ccg gag acc atc ggc agg cga gtg gct gtg gga ctc ggg tcc tgc ctc	1591
Pro Glu Thr Ile Gly Arg Arg Val Ala Val Gly Leu Gly Ser Cys Leu	
505 510 515	
gcc atc ctc atc ctg gca atc tgt ggg ctc aag ctc cag cga cgt tgg	1639
Ala Ile Leu Ile Leu Ala Ile Cys Gly Leu Lys Leu Gln Arg Arg Trp	
520 525 530 535	
aag agg aca cag agc cag cag ggg ctt cag gag aat tcc agc ggc cag	1687
Lys Arg Thr Gln Ser Gln Gln Gly Leu Gln Glu Asn Ser Ser Gly Gln	
540 545 550	
agc ttc ttt gtg agg aat aaa aag gtt aga agg gcc ccc ctc tct gaa	1735
Ser Phe Phe Val Arg Asn Lys Lys Val Arg Arg Ala Pro Leu Ser Glu	
555 560 565	
ggc ccc cac tcc ctg gga tgc tac aat cca atg atg gaa gat ggc att	1783
Gly Pro His Ser Leu Gly Cys Tyr Asn Pro Met Met Glu Asp Gly Ile	
570 575 580	
agc tac acc acc ctg cgc ttt ccc gag atg aac ata cca cga act gga	1831
Ser Tyr Thr Thr Leu Arg Phe Pro Glu Met Asn Ile Pro Arg Thr Gly	
585 590 595	

gat gca gag tcc tca gag atg cag aga cct ccc ccg gac tgc gat gac 1879
Asp Ala Glu Ser Ser Glu Met Gln Arg Pro Pro Pro Asp Cys Asp Asp
600 605 610 615

acg gtc act tat tca gca ttg cac aag cgc caa gtg ggc act atg aga 1927
Thr Val Thr Tyr Ser Ala Leu His Lys Arg Gln Val Gly Thr Met Arg
620 625 630

acg tca ttc cag att ttc cag aag atg agg gga ttc att act cag agc 1975
Thr Ser Phe Gln Ile Phe Gln Lys Met Arg Gly Phe Ile Thr Gln Ser
635 640 645

tgatccagtt tggggtcggg gagcggcctc aggcacaaga aaatgtggac tatgtgatcc 2035
tcaaacattg acactggatg ggctgcagca gaggcactgg gggcagcggg ggccagggaa 2095
gtccccgagt tt 2107

<210> 27
<211> 647
<212> PRT
<213> Homo sapiens

<400> 27
Met His Leu Leu Gly Pro Trp Leu Leu Leu Leu Val Leu Glu Tyr Leu
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Ala Phe Ser Asp Ser Ser Lys Trp Val Phe Glu His Pro Glu Thr Leu
20 25 30

Tyr Ala Trp Glu Gly Ala Cys Val Trp Ile Pro Cys Thr Tyr Arg Ala
35 40 45

Leu Asp Gly Asp Leu Glu Ser Phe Ile Leu Phe His Asn Pro Glu Tyr
50 55 60

Asn Lys Asn Thr Ser Lys Phe Asp Gly Thr Arg Leu Tyr Glu Ser Thr
65 70 75 80

Lys Asp Gly Lys Val Pro Ser Glu Gln Lys Arg Val Gln Phe Leu Gly
85 90 95

Asp Lys Asn Lys Asn Cys Thr Leu Ser Ile His Pro Val His Leu Asn
100 105 110

Asp Ser Gly Gln Leu Gly Leu Arg Met Glu Ser Lys Thr Glu Lys Trp
115 120 125

Met Glu Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His
130 135 140

Ile Gln Leu Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr
145 150 155 160

Cys Leu Leu Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp
 165 170 175
 Leu Leu Glu Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser
 180 185 190
 Leu Thr Ile Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro
 195 200 205
 Gln Trp Ser His His Gly Lys Ile Val Thr Cys Gln Leu Gln Asp Ala
 210 215 220
 Asp Gly Lys Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His
 225 230 235 240
 Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile Arg
 245 250 255
 Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn Pro
 260 265 270
 Ser Val Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu Pro
 275 280 285
 Ser Leu Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr Thr
 290 295 300
 Ile Ala Cys Ala Ala Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro Val
 305 310 315 320
 Ala Leu Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys Ile
 325 330 335
 Lys Pro Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln Cys
 340 345 350
 Asp Phe Ser Ser Ser His Pro Lys Glu Val Gln Phe Phe Trp Glu Lys
 355 360 365
 Asn Gly Arg Leu Leu Gly Lys Glu Ser Gln Leu Asn Phe Asp Ser Ile
 370 375 380
 Ser Pro Glu Asp Ala Gly Ser Tyr Ser Cys Trp Val Asn Asn Ser Ile
 385 390 395 400
 Gly Gln Thr Ala Ser Lys Ala Trp Thr Leu Glu Val Leu Tyr Ala Pro
 405 410 415
 Arg Arg Leu Arg Val Ser Met Ser Pro Gly Asp Gln Val Met Glu Gly
 420 425 430
 Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val Ser
 435 440 445

His Tyr Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro Tyr His Ser
 450 455 460

Gln Lys Leu Arg Leu Glu Pro Val Lys Val Gln His Ser Gly Ala Tyr
 465 470 475 480

Trp Cys Gln Gly Thr Asn Ser Val Gly Lys Gly Arg Ser Pro Leu Ser
 485 490 495

Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Arg Arg Val Ala
 500 505 510

Val Gly Leu Gly Ser Cys Leu Ala Ile Leu Ile Leu Ala Ile Cys Gly
 515 520 525

Leu Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly Leu
 530 535 540

Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys Val
 545 550 555 560

Arg Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr Asn
 565 570 575

Pro Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro Glu
 580 585 590

Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln Arg
 595 600 605

Pro Pro Pro Asp Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His Lys
 610 615 620

Arg Gln Val Gly Thr Met Arg Thr Ser Phe Gln Ile Phe Gln Lys Met
 625 630 635 640

Arg Gly Phe Ile Thr Gln Ser
 645

<210> 28
 <211> 1201
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (101)..(880)

<400> 28
 ggggtgcaaa gaagagacag cagcgcccag cttggaggtg ctaactccag aggccagcat 60
 cagcaactgg gcacagaaag gagccgcctg ggcagggacc atg gca cgg cca cat 115
 Met Ala Arg Pro His
 1 5

ccc tgg tgg ctg tgc gtt ctg ggg acc ctg gtg ggg ctc tca gct act	163
Pro Trp Trp Leu Cys Val Leu Gly Thr Leu Val Gly Leu Ser Ala Thr	
10 15 20	
cca gcc ccc aag agc tgc cca gag agg cac tac tgg gct cag gga aag	211
Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr Trp Ala Gln Gly Lys	
25 30 35	
ctg tgc tgc cag atg tgt gag cca gga aca ttc ctc gtg aag gac tgt	259
Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe Leu Val Lys Asp Cys	
40 45 50	
gac cag cat aga aag gct gct cag tgt gat cct tgc ata ccg ggg gtc	307
Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro Cys Ile Pro Gly Val	
55 60 65	
tcc ttc tct cct gac cac cac acc cgg ccc cac tgt gag agc tgt cgg	355
Ser Phe Ser Pro Asp His His Thr Arg Pro His Cys Glu Ser Cys Arg	
70 75 80 85	
cac tgt aac tct ggt ctt ctc gtt cgc aac tgc acc atc act gcc aat	403
His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys Thr Ile Thr Ala Asn	
90 95 100	
gct gag tgt gcc tgt cgc aat ggc tgg cag tgc agg gac aag gag tgc	451
Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys Arg Asp Lys Glu Cys	
105 110 115	
acc gag tgt gat cct ctt cca aac cct tcg ctg acc gct cgg tcg tct	499
Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu Thr Ala Arg Ser Ser	
120 125 130	
cag gcc ctg agc cca cac cct cag ccc acc cac tta cct tat gtc agt	547
Gln Ala Leu Ser Pro His Pro Gln Pro Thr His Leu Pro Tyr Val Ser	
135 140 145	
gag atg ctg gag gcc agg aca gct ggg cac atg cag act ctg gct gac	595
Glu Met Leu Glu Ala Arg Thr Ala Gly His Met Gln Thr Leu Ala Asp	
150 155 160 165	
ttc agg cag ctg cct gcc cgg act ctc tct acc cac tgg cca ccc caa	643
Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr His Trp Pro Pro Gln	
170 175 180	
aga tcc ctg tgc agc tcc gat ttt att cgc atc ctt gtg atc ttc tct	691
Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile Leu Val Ile Phe Ser	
185 190 195	
gga atg ttc ctt gtt ttc acc ctg gcc ggg gcc ctg ttc ctc cat caa	739
Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala Leu Phe Leu His Gln	
200 205 210	

cga agg aaa tat aga tca aac aaa gga gaa agt cct gtg gag cct gca 787
 Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser Pro Val Glu Pro Ala
 215 220 225
 gag cct tgt cgt tac agc tgc ccc agg gag gag gag ggc agc acc atc 835
 Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu Glu Gly Ser Thr Ile
 230 235 240 245
 ccc atc cag gag gat tac cga aaa ccg gag cct gcc tgc tcc ccc 880
 Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro Ala Cys Ser Pro
 250 255 260
 tgagccagca cctgcggtag ctgcactaca gccctggcct ccacccccac cccgccgacc 940
 atccaaggga gaggtagacc tggcagccac aactgcagtc ccacccctctt gtcagggccc 1000
 tttcctgtgt acacgtgaca gagggccttt tcgagactgg cagggacgag gacaaatatg 1060
 gatgaggtgg agagtgggaa gcaggagccc agccagctgc gcctgcgctg caggagggcg 1120
 ggggctctgg ttgtaaaaca cacttcctgc tgcgaaagac ccacatgcta caagacgggc 1180
 aaaataaagt gacagatgac c 1201

<210> 29
 <211> 260
 <212> PRT
 <213> Homo sapiens

<400> 29
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 1 5 10 15
 Gly Leu Ser Ala Thr Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr
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 Trp Ala Gln Gly Lys Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe
 35 40 45
 Leu Val Lys Asp Cys Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro
 50 55 60
 Cys Ile Pro Gly Val Ser Phe Ser Pro Asp His His Thr Arg Pro His
 65 70 75 80
 Cys Glu Ser Cys Arg His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys
 85 90 95
 Thr Ile Thr Ala Asn Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys
 100 105 110
 Arg Asp Lys Glu Cys Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu
 115 120 125

Thr Ala Arg Ser Ser Gln Ala Leu Ser Pro His Pro Gln Pro Thr His
 130 135 140
 Leu Pro Tyr Val Ser Glu Met Leu Glu Ala Arg Thr Ala Gly His Met
 145 150 155 160
 Gln Thr Leu Ala Asp Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr
 165 170 175
 His Trp Pro Pro Gln Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile
 180 185 190
 Leu Val Ile Phe Ser Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala
 195 200 205
 Leu Phe Leu His Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser
 210 215 220
 Pro Val Glu Pro Ala Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu
 225 230 235 240
 Glu Gly Ser Thr Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro
 245 250 255
 Ala Cys Ser Pro
 260

<210> 30
 <211> 2350
 <212> DNA
 <213> Homo sapiens

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 gagggactta tggaacatct tcaagttgtg ggggtggaca atgctctgtt gtgatttcct 180
 ggcacatcat ggaaccgact gctggactta ccattattct gaaaaaccca tgaactggca 240
 aagggtctaga agattctgcc gagacaatta cacagattta gttgccatac aaaacaaggc 300
 ggaaattgag tatctggaga agactctgcc ttccagtcgt tcttactact ggataggaat 360
 ccggaagata ggaggaatat ggacgtgggt gggaaccaac aaatctctca ctgaagaagc 420
 agagaactgg ggagatggtg agcccaacaa caagaagaac aaggaggact gcgtggagat 480
 ctatatcaag agaaacaaag atgcaggcaa atggaacgat gacgcctgcc acaaactaaa 540
 ggcagccctc tgttacacag cttcttgcca gccctggtea tgcagtggcc atggagaatg 600
 ttagaaaatc atcaataatt acacctgcaa ctgtgatgtg ggggtactatg ggccccagtg 660

tcagtttgtg attcagtgtg agcctttgga ggccccagag ctgggtacca tggactgtac 720
 tcaactcttg ggaaacttca gtttcagctc acagtgtgcc ttcagctgct ctgaaggaac 780
 aaacttaact gggattgaag aaaccacctg tggaccattt ggaaactggc catctccaga 840
 accaacctgt caagtgattc agtgtgagcc tctatcagca ccagatttgg ggatcatgaa 900
 ctgtagccat cccctggcca gtttcagctt tacctctgca tgtaccttca tctgctcaga 960
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 taacccccctc ttcattccag tggcagtcac ggttactgca ttctctgggt tggcatttat 1140
 catttggctg gcaaggagat taaaaaaagg caagaaatcc aagagaagta tgaatgaccc 1200
 atattaaatc gcccttgggtg aaagaaaatt cttggaatac taaaaatcat gagatccttt 1260
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 cccctcattt atccctcaac cccagccca cagggtgtta tacagctcag ctttttgtct 1440
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 gctgactttg ctctttcttg actcttgttt tcagtttcaa ttcagtgtg tacttgatga 1560
 cagacacttc taaatgaagt gcaaatttga tacatatgtg aatatggact cagttttctt 1620
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 aaaaagtcta cgctctcctt tctttctaac tccagtgaag taatggggtc ctgctcaagt 1740
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 tggcttcagc ctccccacct tcttcagcca cctctctttt tcagttggct gacttcaca 1860
 cctagcatct catgagtgcc aagcaaaagg agagaagaga gaaatagcct gcgctgtttt 1920
 ttagtttggg ggttttgctg tttcctttta tgagacccat tcctatttct tatagtcaat 1980
 gtttctttta tcacgatatt attagtaaga aaacatcact gaaatgctag ctgcaagtga 2040
 catctctttg atgtcatatg gaagagttaa aacagggtga gaaattcctt gattcacaat 2100
 gaaatgctct cctttcccct gccccagac cttttatccg acttacctag attctacata 2160
 ttctttaaat ttcattcag gcctccctca accccaccac ttcttttata actagtcctt 2220
 tactaatcca acccatgatg agctcctctt cctggcttct tactgaaagg ttaccctgta 2280

acatgcaatt ttgcatttga ataaagcctg ctttttaagt gttaaaaaaa aaaaaaaaaa 2340

aaaaaaaaaa

2350

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<212> DNA
<213> Homo sapiens

<220>
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<222> (116)..(1198)

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cgcccaggga tctccagct cctttcgccc gcgccctccg ttcgctccgg acacc atg 118
Met
1

gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg 166
Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu
5 10 15

agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta 214
Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val
20 25 30

ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc 262
Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala
35 40 45

gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag 310
Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln
50 55 60 65

atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc 358
Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe
70 75 80

ata gaa ggg cat gtg gtg att ccc cgg atc cac ccc aac tcc atc tgt 406
Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys
85 90 95

gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag 454
Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln
100 105 110

tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt 502
Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys
115 120 125

aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att acc ata	550
Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile	
130 135 140 145	
act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac	598
Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr	
150 155 160	
aga acg aat cct gaa gac atc tac ccc agc aac cct act gat gat gac	646
Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp	
165 170 175	
gtg agc agc ggc tcc tcc agt gaa agg agc agc act tca gga ggt tac	694
Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr	
180 185 190	
atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa gac agt	742
Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser	
195 200 205	
ccc tgg atc acc gac agc aca gac aga atc cct gct acc aga gac caa	790
Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp Gln	
210 215 220 225	
gac aca ttc cac ccc agt ggg ggg tcc cat acc act cat gaa tct gaa	838
Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Glu Ser Glu	
230 235 240	
tca gat gga cac tca cat ggg agt caa gaa ggt gga gca aac aca acc	886
Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr Thr	
245 250 255	
tct ggt cct ata agg aca ccc caa att cca gaa tgg ctg atc atc ttg	934
Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile Leu	
260 265 270	
gca tcc ctc ttg gcc ttg gct ttg att ctt gca gtt tgc att gca gtc	982
Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala Val	
275 280 285	
aac agt cga aga agg tgt ggg cag aag aaa aag cta gtg atc aac agt	1030
Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn Ser	
290 295 300 305	
ggc aat gga gct gtg gag gac aga aag cca agt gga ctc aac gga gag	1078
Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly Glu	
310 315 320	
gcc agc aag tct cag gaa atg gtg cat ttg gtg aac aag gag tcg tca	1126
Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser Ser	
325 330 335	
gaa act cca gac cag ttt atg aca gct gat gag aca agg aac ctg cag	1174
Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu Gln	
340 345 350	

aat gtg gac atg aag att ggg gtg taacacctac accattatct tggaaagaaa 1228
 Asn Val Asp Met Lys Ile Gly Val
 355 360

caaccgttgt aaacataacc attacagga gctgggacac ttaacagatg caatgtgcta 1288
 ctgattgttt cattgcgaat ctttttagc ataaaatttt ctactctttt tgttaaaaaa 1348
 aaaaaa 1354

<210> 32
 <211> 361
 <212> PRT
 <213> Homo sapiens

<400> 32
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 20 25 30
 Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
 35 40 45
 Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
 50 55 60
 Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
 65 70 75 80
 Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
 85 90 95
 Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser
 100 105 110
 Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
 115 120 125
 Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr
 130 135 140
 Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu
 145 150 155 160
 Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp
 165 170 175
 Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
 180 185 190

Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
 195 200 205

Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp
 210 215 220

Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Glu Ser
 225 230 235 240

Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr
 245 250 255

Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile
 260 265 270

Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala
 275 280 285

Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn
 290 295 300

Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly
 305 310 315 320

Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser
 325 330 335

Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu
 340 345 350

Gln Asn Val Asp Met Lys Ile Gly Val
 355 360

<210> 33
 <211> 2308
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (116)..(1594)

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cgcccaggga tcctccagct cctttcgccc gcgccctccg ttcgctccgg acacc atg 118
 Met
 1

gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg 166
 Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu
 5 10 15

agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta 214
 Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val
 20 25 30

ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc 262
 Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala
 35 40 45

gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag 310
 Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln
 50 55 60 65

atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc 358
 Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe
 70 75 80

ata gaa ggg cat gtg gtg att ccc cgg atc cac ccc aac tcc atc tgt 406
 Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys
 85 90 95

gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag 454
 Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln
 100 105 110

tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt 502
 Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys
 115 120 125

aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att acc ata 550
 Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile
 130 135 140 145

act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac 598
 Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr
 150 155 160

aga acg aat cct gaa gac atc tac ccc agc aac cct act gat gat gac 646
 Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp
 165 170 175

gtg agc agc ggc tcc tcc agt gaa agg agc agc act tca gga ggt tac 694
 Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr
 180 185 190

atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa gac agt 742
 Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser
 195 200 205

ccc tgg atc acc gac agc aca gac aga atc cct cgt acc aat atg gac 790
 Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Arg Thr Asn Met Asp
 210 215 220 225

tcc agt cat agt aca acg ctt cag cct act gca aat cca aac aca ggt 838
 Ser Ser His Ser Thr Thr Leu Gln Pro Thr Ala Asn Pro Asn Thr Gly
 230 235 240

ttg gtg gaa gat ttg gac agg aca gga cct ctt tca atg aca acg cag	886
Leu Val Glu Asp Leu Asp Arg Thr Gly Pro Leu Ser Met Thr Thr Gln	
245 250 255	
cag agt aat tct cag agc ttc tct aca tca cat gaa ggc ttg gaa gaa	934
Gln Ser Asn Ser Gln Ser Phe Ser Thr Ser His Glu Gly Leu Glu Glu	
260 265 270	
gat aaa gac cat cca aca act tct act ctg aca tca agc aat agg aat	982
Asp Lys Asp His Pro Thr Thr Ser Thr Leu Thr Ser Ser Asn Arg Asn	
275 280 285	
gat gtc aca ggt gga aga aga gac cca aat cat tct gaa ggc tca act	1030
Asp Val Thr Gly Gly Arg Arg Asp Pro Asn His Ser Glu Gly Ser Thr	
290 295 300 305	
cat tta ctg gaa ggt tat acc tct cat tac cca cac acg aag gaa agc	1078
His Leu Leu Glu Gly Tyr Thr Ser His Tyr Pro His Thr Lys Glu Ser	
310 315 320	
agg acc ttc atc cca gtg acc tca gct aag act ggg tcc ttt gga gtt	1126
Arg Thr Phe Ile Pro Val Thr Ser Ala Lys Thr Gly Ser Phe Gly Val	
325 330 335	
act gca gtt act gtt gga gat tcc aac tct aat gtc aat cgt tcc tta	1174
Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn Val Asn Arg Ser Leu	
340 345 350	
tca gga gac caa gac aca ttc cac ccc agt ggg ggg tcc cat acc act	1222
Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr	
355 360 365	
cat gga tct gaa tca gat gga cac tca cat ggg agt caa gaa ggt gga	1270
His Gly Ser Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly	
370 375 380 385	
gca aac aca acc tct ggt cct ata agg aca ccc caa att cca gaa tgg	1318
Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp	
390 395 400	
ctg atc atc ttg gca tcc ctc ttg gcc ttg gct ttg att ctt gca gtt	1366
Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val	
405 410 415	
tgc att gca gtc aac agt cga aga agg tgt ggg cag aag aaa aag cta	1414
Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu	
420 425 430	
gtg atc aac agt ggc aat gga gct gtg gag gac aga aag cca agt gga	1462
Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly	
435 440 445	

ctc aac gga gag gcc agc aag tct cag gaa atg gtg cat ttg gtg aac 1510
 Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn 465
 450 455 460

aag gag tcg tca gaa act cca gac cag ttt atg aca gct gat gag aca 1558
 Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr 480
 470 475

agg aac ctg cag aat gtg gac atg aag att ggg gtg taacacctac 1604
 Arg Asn Leu Gln Asn Val Asp Met Lys Ile Gly Val 490
 485

accattatct tggaaagaaa caacgttggg aacataacca ttacagggga gctgggacac 1664
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 aatagggcct ggtcctggga ggaaatttga atgggtcatt ttgcccttcc attagcctaa 2024
 tccctgggca ttgctttcca ctgagggttg gggttggggg gtactagtta cacatcttca 2084
 acagaccccc tctagaaatt tttcagatgc ttctgggaga cacccaaagg gtaagtctat 2144
 ttatctgtag taaactattt atctgtgttt ttgaaatatt aaaccctgga tcagtccttt 2204
 tattcagtat aattttttta agttactttg tcagaggcac aaaaagggtt taaactgatt 2264
 cataataaat atctgtacct tcttcgaaaa aaaaaaaaaa aaaa 2308

<210> 34
 <211> 493
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro 15
 1 5 10

Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly 30
 20 25

Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu 45
 35 40

Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala 60
 50 55

Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
 65 70 75 80
 Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
 85 90 95
 Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser
 100 105 110
 Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
 115 120 125
 Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr
 130 135 140
 Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu
 145 150 155 160
 Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp
 165 170 175
 Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
 180 185 190
 Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
 195 200 205
 Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Arg Thr Asn Met
 210 215 220
 Asp Ser Ser His Ser Thr Thr Leu Gln Pro Thr Ala Asn Pro Asn Thr
 225 230 235 240
 Gly Leu Val Glu Asp Leu Asp Arg Thr Gly Pro Leu Ser Met Thr Thr
 245 250 255
 Gln Gln Ser Asn Ser Gln Ser Phe Ser Thr Ser His Glu Gly Leu Glu
 260 265 270
 Glu Asp Lys Asp His Pro Thr Thr Ser Thr Leu Thr Ser Ser Asn Arg
 275 280 285
 Asn Asp Val Thr Gly Gly Arg Arg Asp Pro Asn His Ser Glu Gly Ser
 290 295 300
 Thr His Leu Leu Glu Gly Tyr Thr Ser His Tyr Pro His Thr Lys Glu
 305 310 315 320
 Ser Arg Thr Phe Ile Pro Val Thr Ser Ala Lys Thr Gly Ser Phe Gly
 325 330 335
 Val Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn Val Asn Arg Ser
 340 345 350

Leu Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr
 355 360 365

Thr His Gly Ser Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly
 370 375 380

Gly Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu
 385 390 395 400

Trp Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala
 405 410 415

Val Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys
 420 425 430

Leu Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser
 435 440 445

Gly Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val
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 Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val
 1 5 10

ctg ttt ttc ttc aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg 157
 Leu Phe Phe Phe Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu
 15 20 25

ggc ttt ggg atc tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc 205
 Gly Phe Gly Ile Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe
 30 35 40

cat aac ctc ccc tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc 253
 His Asn Leu Pro Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly
 45 50 55 60

tct att atc atg gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag 301
Ser Ile Ile Met Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys
65 70 75

gaa aac aag tgt ctg ctt atg tcg ttc ttc atc ctg ctg ctg att atc 349
Glu Asn Lys Cys Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile
80 85 90

ctc ctt gct gag gtg acc ttg gcc atc ctg ctc ttt gta tat gaa cag 397
Leu Leu Ala Glu Val Thr Leu Ala Ile Leu Leu Phe Val Tyr Glu Gln
95 100 105

aag ctg aat gag tat gtg gct aag ggt ctg acc gac agc atc cac cgt 445
Lys Leu Asn Glu Tyr Val Ala Lys Gly Leu Thr Asp Ser Ile His Arg
110 115 120

tac cac tca gac aat agc acc aag gca gcg tgg gac tcc atc cag tca 493
Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser Ile Gln Ser
125 130 135 140

ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg acc agt ggc 541
Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp Thr Ser Gly
145 150 155

cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt tgc tat gcg 589
Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly Cys Tyr Ala
160 165 170

aaa gca aga ctg tgg ttt cat tcc aat ttc ctg tat atc gga atc atc 637
Lys Ala Arg Leu Trp Phe His Ser Asn Phe Leu Tyr Ile Gly Ile Ile
175 180 185

acc atc tgt gta tgt gtg att gag gtg ttg ggg atg tcc ttt gca ctg 685
Thr Ile Cys Val Cys Val Ile Glu Val Leu Gly Met Ser Phe Ala Leu
190 195 200

acc ctg aac tgc cag att gac aaa acc agc cag acc ata ggg cta 730
Thr Leu Asn Cys Gln Ile Asp Lys Thr Ser Gln Thr Ile Gly Leu
205 210 215

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 Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
 35 40 45
 Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
 50 55 60
 Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
 65 70 75 80
 Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
 85 90 95
 Val Thr Leu Ala Ile Leu Leu Phe Val Tyr Glu Gln Lys Leu Asn Glu
 100 105 110
 Tyr Val Ala Lys Gly Leu Thr Asp Ser Ile His Arg Tyr His Ser Asp
 115 120 125
 Asn Ser Thr Lys Ala Ala Trp Asp Ser Ile Gln Ser Phe Leu Gln Cys
 130 135 140
 Cys Gly Ile Asn Gly Thr Ser Asp Trp Thr Ser Gly Pro Pro Ala Ser
 145 150 155 160
 Cys Pro Ser Asp Arg Lys Val Glu Gly Cys Tyr Ala Lys Ala Arg Leu
 165 170 175
 Trp Phe His Ser Asn Phe Leu Tyr Ile Gly Ile Ile Thr Ile Cys Val
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Cys Val Ile Glu Val Leu Gly Met Ser Phe Ala Leu Thr Leu Asn Cys
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Oligonucleotide primer

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